RAW SEQUENCE LISTING
PATENT APPLICATION *US/09/055,145A*

DATE: 10/26/98
TIME: 11:25:12

INPUT SET: S29430.raw

This Raw Listing contains the General Information Section and up to the first 5 pages.

SEQUENCE LISTING

(1) General Information:

(i) APPLICANT: Weeks, Donald P.
Wang, Xiao-Zhuo
Herman, Patricia L.

(ii) TITLE OF INVENTION: "METHODS AND MATERIALS FOR MAKING AND USING TRANSGENIC DICAMBA-DEGRADING ORGANISMS"

(iii) NUMBER OF SEQUENCES: 6

(iv) CORRESPONDENCE ADDRESS:
(A) ADDRESSEE: Sheridan Ross P.C.
(B) STREET: 1700 Lincoln St., Suite 3500
(C) CITY: Denver
(D) STATE: Colorado
(E) COUNTRY: USA
(F) ZIP: 80203

(v) COMPUTER READABLE FORM:
(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30

(vi) CURRENT APPLICATION DATA:
(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/042,666
(B) FILING DATE: 04-APR-1997

(vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 60/042,941
(B) FILING DATE: 04-APR-1997

(viii) ATTORNEY/AGENT INFORMATION:
(A) NAME: Crook, Wannell M.
(B) REGISTRATION NUMBER: 31,071
(C) REFERENCE/DOCKET NUMBER: 3553-18

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: (303) 863-9700
(B) TELEFAX: (303) 863-0223

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
(A) NAME/KEY: Region
(B) LOCATION: 28
(D) OTHER INFORMATION: /note= "Best guess for Xaa = Asp or Thr"

(ix) FEATURE:
(A) NAME/KEY: Region
(B) LOCATION: 29
(D) OTHER INFORMATION: /note= "Best guess for Xaa = Pro"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
Thr Phe Val Arg Asn Ala Trp Tyr Val Ala Ala Leu Pro Glu Glu Leu
1               5                  10                  15

Ser Glu Lys Pro Leu Gly Arg Thr Ile Leu Asp Xaa Xaa
            20                  25
```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(ix) FEATURE:
(A) NAME/KEY: Region
(B) LOCATION: 8
(D) OTHER INFORMATION: /note= "Best guess for Xaa = Cys"

(ix) FEATURE:
(A) NAME/KEY: Region

(B) LOCATION: 11
(D) OTHER INFORMATION: /note= "Best guess for Xaa = Cys"

(ix) FEATURE:
(A) NAME/KEY: Region
(B) LOCATION: 16
(D) OTHER INFORMATION: /note= "Best guess for Xaa = Cys"

(ix) FEATURE:
(A) NAME/KEY: Region
(B) LOCATION: 20
(D) OTHER INFORMATION: /note= "Best guess for Xaa = Cys"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Thr Tyr Val Val Thr Asp Ala Xaa Ile Lys Xaa Lys Tyr Met Asp Xaa
1               5                  10                  15

Val Glu Val Xaa
            20
```

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1020 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:
(A) NAME/KEY: CDS
(B) LOCATION: 1..1020

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
ATG ACC TTC GTC CGC AAT GCC TGG TAT GTG GCG GCG CTG CCC GAG GAA        48
Met Thr Phe Val Arg Asn Ala Trp Tyr Val Ala Ala Leu Pro Glu Glu
  1               5                  10                  15

CTG TCC GAA AAG CCG CTC GGC CGG ACG ATT CTC GAC ACA CCG CTC GCG        96
Leu Ser Glu Lys Pro Leu Gly Arg Thr Ile Leu Asp Thr Pro Leu Ala
            20                  25                  30

CTC TAC CGC CAG CCC GAC GGT GTG GTC GCG GCG CTG CTC GAC ATC TGT       144
Leu Tyr Arg Gln Pro Asp Gly Val Val Ala Ala Leu Leu Asp Ile Cys
        35                  40                  45

CCG CAC CGC TTC GCG CCG CTG AGC GAC GGC ATC CTC GTC AAC GGC CAT       192
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```
153  Pro His Arg Phe Ala Pro Leu Ser Asp Gly Ile Leu Val Asn Gly His
154       50                  55                  60
155
156  CTC CAA TGC CCC TAT CAC GGG CTG GAA TTC GAT GGC GGC GGG CAG TGC        240
157  Leu Gln Cys Pro Tyr His Gly Leu Glu Phe Asp Gly Gly Gly Gln Cys
158   65                  70                  75                  80
159
160  GTC CAT AAC CCG CAC GGC AAT GGC GCC CGC CCG GCT TCG CTC AAC GTC        288
161  Val His Asn Pro His Gly Asn Gly Ala Arg Pro Ala Ser Leu Asn Val
162                  85                  90                  95
163
164  CGC TCC TTC CCG GTG GTG GAG CGC GAC GCG CTG ATC TGG ATC TGG CCC        336
165  Arg Ser Phe Pro Val Val Glu Arg Asp Ala Leu Ile Trp Ile Trp Pro
166              100                 105                 110
167
168  GGC GAT CCG GCG CTG GCC GAT CCT GGG GCG ATC CCC GAC TTC GGC TGC        384
169  Gly Asp Pro Ala Leu Ala Asp Pro Gly Ala Ile Pro Asp Phe Gly Cys
170          115                 120                 125
171
172  CGC GTC GAT CCC GCC TAT CGG ACC GTC GGC GGC TAT GGG CAT GTC GAC        432
173  Arg Val Asp Pro Ala Tyr Arg Thr Val Gly Gly Tyr Gly His Val Asp
174      130                 135                 140
175
176  TGC AAC TAC AAG CTG CTG GTC GAC AAC CTG ATG GAC CTC GGC CAC GCC        480
177  Cys Asn Tyr Lys Leu Leu Val Asp Asn Leu Met Asp Leu Gly His Ala
178  145                 150                 155                 160
179
180  CAA TAT GTC CAT CGC GCC AAC GCC CAG ACC GAC GCC TTC GAC CGG CTG        528
181  Gln Tyr Val His Arg Ala Asn Ala Gln Thr Asp Ala Phe Asp Arg Leu
182                  165                 170                 175
183
184  GAG CGC GAG GTG ATC GTC GGC GAC GGT GAG ATA CAG GCG CTG ATG AAG        576
185  Glu Arg Glu Val Ile Val Gly Asp Gly Glu Ile Gln Ala Leu Met Lys
186              180                 185                 190
187
188  ATT CCC GGC GGC ACG CCG AGC GTG CTG ATG GCC AAG TTC CTG CGC GGC        624
189  Ile Pro Gly Gly Thr Pro Ser Val Leu Met Ala Lys Phe Leu Arg Gly
190          195                 200                 205
191
192  GCC AAT ACC CCC GTC GAC GCT TGG AAC GAC ATC CGC TGG AAC AAG GTG        672
193  Ala Asn Thr Pro Val Asp Ala Trp Asn Asp Ile Arg Trp Asn Lys Val
194      210                 215                 220
195
196  AGC GCG ATG CTC AAC TTC ATC GCG GTG GCG CCG GAA GGC ACC CCG AAG        720
197  Ser Ala Met Leu Asn Phe Ile Ala Val Ala Pro Glu Gly Thr Pro Lys
198  225                 230                 235                 240
199
200  GAG CAG AGC ATC CAC TCG CGC GGT ACC CAT ATC CTG ACC CCC GAG ACG        768
201  Glu Gln Ser Ile His Ser Arg Gly Thr His Ile Leu Thr Pro Glu Thr
202                  245                 250                 255
203
204  GAG GCG AGC TGC CAT TAT TTC TTC GGC TCC TCG CGC AAT TTC GGC ATC        816
205  Glu Ala Ser Cys His Tyr Phe Phe Gly Ser Ser Arg Asn Phe Gly Ile
```

```
                260                 265                 270
GAC GAT CCG GAG ATG GAC GGC GTG CTG CGC AGC TGG CAG GCT CAG GCG        864
Asp Asp Pro Glu Met Asp Gly Val Leu Arg Ser Trp Gln Ala Gln Ala
        275                 280                 285

CTG GTC AAG GAG GAC AAG GTC GTC GTC GAG GCG ATC GAG CGC CGC CGC        912
Leu Val Lys Glu Asp Lys Val Val Val Glu Ala Ile Glu Arg Arg Arg
    290                 295                 300

GCC TAT GTC GAG GCG AAT GGC ATC CGC CCG GCG ATG CTG TCG TGC GAC        960
Ala Tyr Val Glu Ala Asn Gly Ile Arg Pro Ala Met Leu Ser Cys Asp
305                 310                 315                 320

GAA GCC GCA GTC CGT GTC AGC CGC GAG ATC GAG AAG CTT GAG CAG CTC       1008
Glu Ala Ala Val Arg Val Ser Arg Glu Ile Glu Lys Leu Glu Gln Leu
                325                 330                 335

GAA GCC GCC TGA                                                      1020
Glu Ala Ala  *
             340


(2) INFORMATION FOR SEQ ID NO:4:

       (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH:  339 amino acids
             (B) TYPE: amino acid
             (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: protein

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Thr Phe Val Arg Asn Ala Trp Tyr Val Ala Ala Leu Pro Glu Glu
  1               5                  10                  15

Leu Ser Glu Lys Pro Leu Gly Arg Thr Ile Leu Asp Thr Pro Leu Ala
            20                  25                  30

Leu Tyr Arg Gln Pro Asp Gly Val Val Ala Ala Leu Leu Asp Ile Cys
        35                  40                  45

Pro His Arg Phe Ala Pro Leu Ser Asp Gly Ile Leu Val Asn Gly His
    50                  55                  60

Leu Gln Cys Pro Tyr His Gly Leu Glu Phe Asp Gly Gly Gly Gln Cys
65                  70                  75                  80

Val His Asn Pro His Gly Asn Gly Ala Arg Pro Ala Ser Leu Asn Val
                85                  90                  95

Arg Ser Phe Pro Val Val Glu Arg Asp Ala Leu Ile Trp Ile Trp Pro
```

SEQUENCE VERIFICATION REPORT
PATENT APPLICATION ***US/09/055,145A***

DATE: 10/26/98
TIME: 11:25:17

INPUT SET: S29430.raw

Line	Error	Original Text
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